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SEQUENCE LISTING

<110> Bureau of Sugar Experiment Stations

The University of Queensland

<120> A bioreactor system

<130> 12272440/EJH

<160> 53

<170> PatentIn version 3.0

<210> 1

<211> 1182

<212> DNA

<213> Rastonia Eutropia

<220>

<221> CDS

<222> (1)..(1182)

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ttt	ggc	ggc	tgc	ctg	gcc	aag	atc	ccg	gca	ccg	gaa	ctg	ggt	gcc	gtg	96
Phe	Gly	Gly	Ser	Leu	Ala	Lys	Ile	Pro	Ala	Pro	Glu	Leu	Gly	Ala	Val	
			20				25					30				

gtc	atc	aag	gcc	gcg	ctg	gag	cgc	gcc	ggc	gtc	aag	ccg	gag	cag	gtg	144
Val	Ile	Lys	Ala	Ala	Leu	Glu	Arg	Ala	Gly	Val	Lys	Pro	Glu	Gln	Val	
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ccc gca cgc cag gcc gcg atc aag gcc ggc ctg ccg gcg atg gtg ccg Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala Met Val Pro 65 70 75 80	240
gcc atg acc atc aac aag gtg tgc ggc tcg ggc ctg aag gcc gtg atg Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met 85 90 95	288
ctg gcc gcc aac gcg atc atg gcg ggc gac gcc gag atc gtg gtg gcc Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile Val Val Ala 100 105 110	336
ggc ggc cag gaa aac atg agc gcc gcc ccg cac gtg ctg ccg ggc tcg Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu Pro Gly Ser 115 120 125	384
cgc gat ggt ttc cgc atg ggc gat gcc aag ctg gtc gac acc atg atc Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp Thr Met Ile 130 135 140	432
gtc gac ggc ctg tgg gac gtg tac aac cag tac cac atg ggc atc acc Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met Gly Ile Thr 145 150 155 160	480
gcc gag aac gtg gcc aag gaa tac ggc atc aca cgc gag gcg cag gat Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu Ala Gln Asp 165 170 175	528
gag ttc gcc gtc ggc tcg cag aac aag gcc gaa gcc gcg cag aag gcc Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala 180 185 190	576
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ggc gac ccg gtg gcc ttc aag acc gac gag ttc gtg cgc cag ggc gcc Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg Gln Gly Ala 210 215 220	672
acg ctg gac agc atg tcc ggc ctc aag ccc gcc ttc gac aag gcc ggc Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp Lys Ala Gly 225 230 235 240	720
acg gtg acc gcg gcc aac gcc tcg ggc ctg aac gac ggc gcc gcc gcg Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly Ala Ala Ala 245 250 255	768
gtg gtg gtg atg tcg gcg gcc aag gcc aag gaa ctg ggc ctg acc ccg Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly Leu Thr Pro 260 265 270	816
ctg gcc acg atc aag agc tat gcc aac gcc ggt gtc gat ccc aag gtg	864

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Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp Pro Lys Val
 275 280 285
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 Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu Ser Arg Ala
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 gag tgg acc ccg caa gac ctg gac ctg atg gag atc aac gag gcc ttt 960
 Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn Glu Ala Phe
 305 310 315 320
 gcc gcc cag gcg ctg gcg gtg cac cag cag atg ggc tgg gac acc tcc 1008
 Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp Asp Thr Ser
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 aag gtc aat gtg aac ggc ggc gcc atc gcc atc ggc cac ccg atc ggc 1056
 Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly
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 gcg tcg ggc tgc cgt atc ctg gtg acg ctg ctg cac gag atg aag cgc 1104
 Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg
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 Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly Gly Gly Met
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<211> 393

<212> PRT

<213> Rastonia Eutropia

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Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro Glu Gln Val
 35 40 45

Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser Gly Gln Asn

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Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met		
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Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile Val Val Ala		
	100	105 110
Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu Pro Gly Ser		
	115	120 125
Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp Thr Met Ile		
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Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met Gly Ile Thr		
145	150	155 160
Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu Ala Gln Asp		
	165	170 175
Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala		
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Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro Gln Arg Lys		
	195	200 205
Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg Gln Gly Ala		
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Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp Lys Ala Gly		
225	230	235 240
Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly Ala Ala Ala		
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Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly Leu Thr Pro		
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Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp Pro Lys Val		
	275	280 285

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Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu Ser Arg Ala
 290 295 300

Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn Glu Ala Phe
 305 310 315 320

Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp Asp Thr Ser
 325 330 335

Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly
 340 345 350

Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg
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Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly Gly Gly Met
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Gly Val Ala Leu Ala Val Glu Arg Lys
 385 390

<210> 3

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<212> DNA

<213> Rastonia Eutropia

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gagcgcgccg gcgtcaagcc ggagcaggtg agcgaagtca tcatgggcca ggtgctgacc	180
gccggttcgg gccagaaccc cgcacgccag gccgcgatca aggccggcct gccggcgatg	240
gtgccggcca tgaccatcaa caaggtgtgc ggctcggggc tgaaggccgt gatgctggcc	300
gccaacgcga tcatggcggg cgacgccgag atcgtggtgg ccggcgcca ggaaaacatg	360
agcgccgcc cgcacgtgct gccgggctcg cgcgatggtt tccgatggg cgatgccaag	420
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atcaccgccg agaacgtggc caaggaatac ggcatacacac gcgaggcgca ggatgagttc 540
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atcgtcccgg tgctgatccc gcagcgcaag ggcgacccgg tggccttcaa gaccgacgag 660
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<211> 738

<212> DNA

<213> Rastonia Eutropia

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<221> CDS

<222> (1)..(738)

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Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
20 25 30

ggt tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg gag cag cag 144

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Lys	Ala	Leu	Gly	Phe	Asp	Phe	Ile	Ala	Ser	Glu	Gly	Asn	Val	Ala	Asp	
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Trp	Asp	Ser	Thr	Lys	Thr	Ala	Phe	Asp	Lys	Val	Lys	Ser	Glu	Val	Gly	
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Glu	Val	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Val	Val	
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ttc	cgc	aag	atg	acc	cgc	gcc	gac	tgg	gat	gcg	gtg	atc	gac	acc	aac	336
Phe	Arg	Lys	Met	Thr	Arg	Ala	Asp	Trp	Asp	Ala	Val	Ile	Asp	Thr	Asn	
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ctg	acc	tcg	ctg	ttc	aac	gtc	acc	aag	cag	gtg	atc	gac	ggc	atg	gcc	384
Leu	Thr	Ser	Leu	Phe	Asn	Val	Thr	Lys	Gln	Val	Ile	Asp	Gly	Met	Ala	
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gac	cgt	ggc	tgg	ggc	cgc	atc	gtc	aac	atc	tcg	tcg	gtg	aac	ggg	cag	432
Asp	Arg	Gly	Trp	Gly	Arg	Ile	Val	Asn	Ile	Ser	Ser	Val	Asn	Gly	Gln	
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aag	ggc	cag	ttc	ggc	cag	acc	aac	tac	tcc	acc	gcc	aag	gcc	ggc	ctg	480
Lys	Gly	Gln	Phe	Gly	Gln	Thr	Asn	Tyr	Ser	Thr	Ala	Lys	Ala	Gly	Leu	
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His	Gly	Phe	Thr	Met	Ala	Leu	Ala	Gln	Glu	Val	Ala	Thr	Lys	Gly	Val	
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acc	gtc	aac	acg	gtc	tct	ccg	ggc	tat	atc	gcc	acc	gac	atg	gtc	aag	576
Thr	Val	Asn	Thr	Val	Ser	Pro	Gly	Tyr	Ile	Ala	Thr	Asp	Met	Val	Lys	
				180					185					190		
gcg	atc	cgc	cag	gac	gtg	ctc	gac	aag	atc	gtc	gcg	acg	atc	ccg	gtc	624
Ala	Ile	Arg	Gln	Asp	Val	Leu	Asp	Lys	Ile	Val	Ala	Thr	Ile	Pro	Val	
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aag	cgc	ctg	ggc	ctg	cca	gaa	gag	atc	gcc	tcg	atc	tgc	gcc	tgg	ttg	672
Lys	Arg	Leu	Gly	Leu	Pro	Glu	Glu	Ile	Ala	Ser	Ile	Cys	Ala	Trp	Leu	
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tcg	tcg	gag	gag	tcc	ggt	ttc	tcg	acc	ggc	gcc	gac	ttc	tcg	ctc	aac	720
Ser	Ser	Glu	Glu	Ser	Gly	Phe	Ser	Thr	Gly	Ala	Asp	Phe	Ser	Leu	Asn	
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Gly	Gly	Leu	His	Met	Gly											
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<211> 246

<212> PRT

<213> Rastonia Eutropia

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 35 40 45

Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
 50 55 60

Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
 65 70 75 80

Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
 85 90 95

Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
 100 105 110

Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
 115 120 125

Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
 130 135 140

Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
 145 150 155 160

His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
 165 170 175

Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys

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Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val		
195	200	205
Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu		
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Gly Gly Leu His Met Gly		
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<212> DNA

<213> Rastonia Eutropia

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ccgcgccgcg aaaagtggct ggagcagcag aaggccctgg gcttcgattt cattgcctcg	180
gaaggcaatg tggctgactg ggactcgacc aagaccgcat tcgacaaggt caagtccgag	240
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gtcaccaagc aggtgatcga cggcatggcc gaccgtggct ggggccgcat cgtcaacatc	420
tcgtcgggtga acgggcagaa gggccagttc ggccagacca actactccac cgccaaggcc	480
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aacacggtct ctccgggcta tatcgccacc gacatggtca aggcgatccg ccaggacgtg	600
ctcgacaaga tcgtcgcgac gatcccgtc aagcgcttg gcttgccaga agagatcgcc	660
tcgatctgcg cctggttgtc gtcggaggag tccggtttct cgaccggcgc cgacttctcg	720
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acc	783

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<210> 7

<211> 1767

<212> DNA

<213> Rastonia Eutropia

<220>

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<222> (1)..(1767)

<400> 7

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Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala Thr Trp Leu	
20 25 30	
gaa tgg tcc cgc cag tgg cag ggc act gaa ggc aac ggc cac gcg gcc	144
Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly His Ala Ala	
35 40 45	
gcg tcc ggc att ccg ggc ctg gat gcg ctg gca ggc gtc aag atc gcg	192
Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val Lys Ile Ala	
50 55 60	
ccg gcg cag ctg ggt gat atc cag cag cgc tac atg aag gac ttc tca	240
Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser	
65 70 75 80	
gcg ctg tgg cag gcc atg gcc gag ggc aag gcc gag gcc acc ggt ccg	288
Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro	
85 90 95	
ctg cac gac cgg cgc ttc gcc ggc gac gca tgg cgc acc aac ctc cca	336
Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro	
100 105 110	
tat cgc ttc gct gcc gcg ttc tac ctg ctc aat gcg cgc gcc ttg acc	384
Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr	
115 120 125	
gag ctg gcc gat gcc gtc gag gcc gat gcc aag acc cgc cag cgc atc	432
Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg Gln Arg Ile	
130 135 140	

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145 150 155 160	
ctt gcc acc aat ccc gag gcg cag cgc ctg ctg atc gag tcg ggc ggc	528
Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu Ser Gly Gly	
165 170 175	
gaa tcg ctg cgt gcc ggc gtg cgc aac atg atg gaa gac ctg aca cgc	576
Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp Leu Thr Arg	
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Gly Lys Ile Ser Gln Thr Asp Glu Ser Ala Phe Glu Val Gly Arg Asn	
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gtc gcg gtg acc gaa ggc gcc gtg gtc ttc gag aac gag tac ttc cag	672
Val Ala Val Thr Glu Gly Ala Val Val Phe Glu Asn Glu Tyr Phe Gln	
210 215 220	
ctg ttg cag tac aag ccg ctg acc gac aag gtg cac gcg cgc ccg ctg	720
Leu Leu Gln Tyr Lys Pro Leu Thr Asp Lys Val His Ala Arg Pro Leu	
225 230 235 240	
ctg atg gtg ccg ccg tgc atc aac aag tac tac atc ctg gac ctg cag	768
Leu Met Val Pro Pro Cys Ile Asn Lys Tyr Tyr Ile Leu Asp Leu Gln	
245 250 255	
ccg gag agc tcg ctg gtg cgc cat gtg gtg gag cag gga cat acg gtg	816
Pro Glu Ser Ser Leu Val Arg His Val Val Glu Gln Gly His Thr Val	
260 265 270	
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Phe Leu Val Ser Trp Arg Asn Pro Asp Ala Ser Met Ala Gly Ser Thr	
275 280 285	
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Trp Asp Asp Tyr Ile Glu His Ala Ala Ile Arg Ala Ile Glu Val Ala	
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cgc gac atc agc ggc cag gac aag atc aac gtg ctc ggc ttc tgc gtg	960
Arg Asp Ile Ser Gly Gln Asp Lys Ile Asn Val Leu Gly Phe Cys Val	
305 310 315 320	
ggc ggc acc att gtc tcg acc gcg ctg gcg gtg ctg gcc gcg cgc ggc	1008
Gly Gly Thr Ile Val Ser Thr Ala Leu Ala Val Leu Ala Ala Arg Gly	
325 330 335	
gag cac ccg gcc gcc agc gtc acg ctg ctg acc acg ctg ctg gac ttt	1056
Glu His Pro Ala Ala Ser Val Thr Leu Leu Thr Thr Leu Leu Asp Phe	
340 345 350	
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Ala Asp Thr Gly Ile Leu Asp Val Phe Val Asp Glu Gly His Val Gln	
355 360 365	
ttg cgc gag gcc acg ctg ggc ggc ggc gcc ggc gcg ccg tgc gcg ctg	1152

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Leu	Arg	Gly	Leu	Glu	Leu	Ala	Asn	Thr	Phe	Ser	Phe	Leu	Arg	Pro	Asn	400
385					390					395					400	
gac	ctg	gtg	tgg	aac	tac	gtg	gtc	gac	aac	tac	ctg	aag	ggc	aac	acg	1248
Asp	Leu	Val	Trp	Asn	Tyr	Val	Val	Asp	Asn	Tyr	Leu	Lys	Gly	Asn	Thr	
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ccg	gtg	ccg	ttc	gac	ctg	ctg	ttc	tgg	aac	ggc	gac	gcc	acc	aac	ctg	1296
Pro	Val	Pro	Phe	Asp	Leu	Leu	Phe	Trp	Asn	Gly	Asp	Ala	Thr	Asn	Leu	
			420					425					430			
ccg	ggg	ccg	tgg	tac	tgc	tgg	tac	ctg	cgc	cac	acc	tac	ctg	cag	aac	1344
Pro	Gly	Pro	Trp	Tyr	Cys	Trp	Tyr	Leu	Arg	His	Thr	Tyr	Leu	Gln	Asn	
		435					440					445				
gag	ctc	aag	gta	ccg	ggc	aag	ctg	acc	gtg	tgc	ggc	gtg	ccg	gtg	gac	1392
Glu	Leu	Lys	Val	Pro	Gly	Lys	Leu	Thr	Val	Cys	Gly	Val	Pro	Val	Asp	
	450					455					460					
ctg	gcc	agc	atc	gac	gtg	ccg	acc	tat	atc	tac	ggc	tcg	cgc	gaa	gac	1440
Leu	Ala	Ser	Ile	Asp	Val	Pro	Thr	Tyr	Ile	Tyr	Gly	Ser	Arg	Glu	Asp	
465					470					475					480	
cat	atc	gtg	ccg	tgg	acc	gcg	gcc	tat	gcc	tcg	acc	gcg	ctg	ctg	gcg	1488
His	Ile	Val	Pro	Trp	Thr	Ala	Ala	Tyr	Ala	Ser	Thr	Ala	Leu	Leu	Ala	
				485					490					495		
aac	aag	ctg	cgc	ttc	gtg	ctg	ggt	gcg	tcg	ggc	cat	atc	gcc	ggt	gtg	1536
Asn	Lys	Leu	Arg	Phe	Val	Leu	Gly	Ala	Ser	Gly	His	Ile	Ala	Gly	Val	
			500					505					510			
atc	aac	ccg	ccg	gcc	aag	aac	aag	cgc	agc	cac	tgg	act	aac	gat	gcg	1584
Ile	Asn	Pro	Pro	Ala	Lys	Asn	Lys	Arg	Ser	His	Trp	Thr	Asn	Asp	Ala	
	515						520					525				
ctg	ccg	gag	tcg	ccg	cag	caa	tgg	ctg	gcc	ggc	gcc	atc	gag	cat	cac	1632
Leu	Pro	Glu	Ser	Pro	Gln	Gln	Trp	Leu	Ala	Gly	Ala	Ile	Glu	His	His	
	530					535					540					
ggc	agc	tgg	tgg	ccg	gac	tgg	acc	gca	tgg	ctg	gcc	ggg	cag	gcc	ggc	1680
Gly	Ser	Trp	Trp	Pro	Asp	Trp	Thr	Ala	Trp	Leu	Ala	Gly	Gln	Ala	Gly	
545					550					555					560	
gcg	aaa	cgc	gcc	gcg	ccc	gcc	aac	tat	ggc	aat	gcg	cgc	tat	cgc	gca	1728
Ala	Lys	Arg	Ala	Ala	Pro	Ala	Asn	Tyr	Gly	Asn	Ala	Arg	Tyr	Arg	Ala	
				565					570					575		
atc	gaa	ccc	gcg	cct	ggg	cga	tac	gtc	aaa	gcc	aag	gca				1767
Ile	Glu	Pro	Ala	Pro	Gly	Arg	Tyr	Val	Lys	Ala	Lys	Ala				
			580					585								

- 13 -

<210> 8

<211> 589

<212> PRT

<213> Rastonia Eutropia

<400> 8

Met Ala Thr Gly Lys Gly Ala Ala Ala Ser Thr Gln Glu Gly Lys Ser
1 5 10 15

Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala Thr Trp Leu
20 25 30

Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly His Ala Ala
35 40 45

Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val Lys Ile Ala
50 55 60

Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser
65 70 75 80

Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro
85 90 95

Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro
100 105 110

Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr
115 120 125

Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg Gln Arg Ile
130 135 140

Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro Ala Asn Phe
145 150 155 160

Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu Ser Gly Gly
165 170 175

Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp Leu Thr Arg

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180							185					190				
Gly	Lys	Ile	Ser	Gln	Thr	Asp	Glu	Ser	Ala	Phe	Glu	Val	Gly	Arg	Asn	
		195					200					205				
Val	Ala	Val	Thr	Glu	Gly	Ala	Val	Val	Phe	Glu	Asn	Glu	Tyr	Phe	Gln	
	210					215					220					
Leu	Leu	Gln	Tyr	Lys	Pro	Leu	Thr	Asp	Lys	Val	His	Ala	Arg	Pro	Leu	
225					230					235					240	
Leu	Met	Val	Pro	Pro	Cys	Ile	Asn	Lys	Tyr	Tyr	Ile	Leu	Asp	Leu	Gln	
				245					250					255		
Pro	Glu	Ser	Ser	Leu	Val	Arg	His	Val	Val	Glu	Gln	Gly	His	Thr	Val	
			260					265					270			
Phe	Leu	Val	Ser	Trp	Arg	Asn	Pro	Asp	Ala	Ser	Met	Ala	Gly	Ser	Thr	
		275					280					285				
Trp	Asp	Asp	Tyr	Ile	Glu	His	Ala	Ala	Ile	Arg	Ala	Ile	Glu	Val	Ala	
	290					295					300					
Arg	Asp	Ile	Ser	Gly	Gln	Asp	Lys	Ile	Asn	Val	Leu	Gly	Phe	Cys	Val	
305					310					315					320	
Gly	Gly	Thr	Ile	Val	Ser	Thr	Ala	Leu	Ala	Val	Leu	Ala	Ala	Arg	Gly	
				325					330					335		
Glu	His	Pro	Ala	Ala	Ser	Val	Thr	Leu	Leu	Thr	Thr	Leu	Leu	Asp	Phe	
			340					345					350			
Ala	Asp	Thr	Gly	Ile	Leu	Asp	Val	Phe	Val	Asp	Glu	Gly	His	Val	Gln	
		355					360					365				
Leu	Arg	Glu	Ala	Thr	Leu	Gly	Gly	Gly	Ala	Gly	Ala	Pro	Cys	Ala	Leu	
	370					375					380					
Leu	Arg	Gly	Leu	Glu	Leu	Ala	Asn	Thr	Phe	Ser	Phe	Leu	Arg	Pro	Asn	
385					390					395					400	
Asp	Leu	Val	Trp	Asn	Tyr	Val	Val	Asp	Asn	Tyr	Leu	Lys	Gly	Asn	Thr	
				405					410					415		

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Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala Thr Asn Leu
 420 425 430

Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr Leu Gln Asn
 435 440 445

Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val Pro Val Asp
 450 455 460

Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser Arg Glu Asp
 465 470 475 480

His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala Leu Leu Ala
 485 490 495

Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile Ala Gly Val
 500 505 510

Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr Asn Asp Ala
 515 520 525

Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile Glu His His
 530 535 540

Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly Gln Ala Gly
 545 550 555 560

Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg Tyr Arg Ala
 565 570 575

Ile Glu Pro Ala Pro Gly Arg Tyr Val Lys Ala Lys Ala
 580 585

<210> 9

<211> 1800

<212> DNA

<213> Rastonia Eutropia

<400> 9

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ggatccatgg cgaccggcaa aggcgcggca gcttcacgc aggaaggcaa gtcccaacca	60
ttcaagggtca cgccggggcc attcgatcca gccacatggc tggaaatggc ccgccagtgg	120
cagggcactg aaggcaacgg ccacgcggcc gcgtccggca ttccgggcct ggatgcgctg	180
gcaggcgctca agatcgcgcc ggcgagctg ggtgatatcc agcagcgcta catgaaggac	240
ttctcagcgc tgtggcaggc catggccgag ggcaaggccg aggccaccgg tccgctgcac	300
gaccggcgct tcgccggcga cgcatggcg accaacctcc catatcgctt cgctgccgcg	360
ttctacctgc tcaatgcgcg cgccttgacc gagctggccg atgccgtcga ggccgatgcc	420
aagacccgcc agcgcatccg cttcgcgatc tcgcaatggg tcgatgcgat gtcgcccgcc	480
aacttccttg ccaccaatcc cgaggcgag cgctgctga tcgagtcggg cggcgaatcg	540
ctgcgtgccg gcgtgcgcaa catgatggaa gacctgacac gcggcaagat ctcgagacc	600
gacgagagcg cgtttgaggt cggccgcaat gtcgcggtga ccgaaggcg cgtggtcttc	660
gagaacgagt acttcagct gttgcagtac aagccgctga ccgacaagg gacgcgcgc	720
ccgctgctga tggtgccgcc gtgcatcaac aagtactaca tcctggacct gcagccggag	780
agctcgctgg tgcgccatgt ggtggagcag ggacatacgg tgtttctggt gtcgtggcg	840
aatccggacg ccagcatggc cggcagcacc tgggacgact acatcgagca cgcgccatc	900
cgcgccatcg aagtcgcgcg cgacatcagc ggccaggaca agatcaacgt gtcggcttc	960
tgcgtgggcg gcaccattgt ctgaccgcg ctggcggtgc tggccgcgcg cggcgagcac	1020
ccggccgcca gcgtcacgct gctgaccag ctgctggact ttgccgacac gggcatcctc	1080
gacgtctttg tcgacgagg ccatgtgcag ttgcgcgagg ccacgctggg cggcggcgcc	1140
ggcgcgccgt gcgcgctgct gcgcggcctt gagctggcca ataccttctc gttcttgcg	1200
ccgaacgacc tgggtgtgaa ctacgtggtc gacaactacc tgaagggcaa cagccgggtg	1260
ccgttcgacc tgctgttctg gaacggcgac gccaccaacc tgccggggcc gtggtactgc	1320
tggtagctgc gccacaccta cctgcagaac gagctcaagg taccgggcaa gctgaccgtg	1380
tgcggcgctgc cggtagacct ggccagcatc gacgtgccga cctatatcta cggctcgcg	1440
gaagaccata tcgtgccgtg gaccgcggcc tatgcctcga ccgcgctgct ggccaacaag	1500
ctgcgcttcg tgctgggtgc gtcgggcat atcgccggtg tgatcaacc gccggccaag	1560
aacaagcgca gccactggac taacgatgcg ctgccggagt cgccgcagca atggctggcc	1620
ggcgccatcg agcatcacg cagctggtgg ccggactgga ccgcatggct ggccgggcag	1680
gccggcgcca aacgcgcgc gcccgccaac tatggcaatg cgcgctatcg cgcaatcgaa	1740

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cccgcgcctg ggcgatacgt caaagccaag gcatgacgct tcaatcgaat tgggggtacc 1800

<210> 10

<211> 1428

<212> DNA

<213> Rastonia Eutropia

<220>

<221> CDS

<222> (1)..(1428)

<400> 10

atg gct tct atg ata tcc tct tcc gct gtg aca aca gtc agc cgt gcc	48
Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala	
1 5 10 15	

tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc	96
Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser	
20 25 30	

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att	144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile	
35 40 45	

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att	192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile	
50 55 60	

gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga	240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg	
65 70 75 80	

gat tcc cgg gtg act gac gtt gtc atc gta tcc gcc gcc cgc acc gcg	288
Asp Ser Arg Val Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala	
85 90 95	

gtc ggc aag ttt ggc ggc tcg ctg gcc aag atc ccg gca ccg gaa ctg	336
Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu	
100 105 110	

ggt gcc gtg gtc atc aag gcc gcg ctg gag cgc gcc ggc gtc aag ccg	384
Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro	
115 120 125	

gag cag gtg agc gaa gtc atc atg ggc cag gtg ctg acc gcc ggt tcg	432
Glu Gln Val Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser	

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130	135	140	
ggc cag aac ccc gca cgc cag gcc gcg atc aag gcc gcc ctg ccg gcg Gly Gln Asn Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala 145 150 155 160			480
atg gtg ccg gcc atg acc atc aac aag gtg tgc gcc tcg gcc ctg aag Met Val Pro Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys 165 170 175			528
gcc gtg atg ctg gcc gcc aac gcg atc atg gcg gcc gac gcc gag atc Ala Val Met Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile 180 185 190			576
gtg gtg gcc gcc gcc cag gaa aac atg agc gcc gcc ccg cac gtg ctg Val Val Ala Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu 195 200 205			624
ccg gcc tcg cgc gat ggt ttc cgc atg gcc gat gcc aag ctg gtc gac Pro Gly Ser Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp 210 215 220			672
acc atg atc gtc gac gcc ctg tgg gac gtg tac aac cag tac cac atg Thr Met Ile Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met 225 230 235 240			720
ggc atc acc gcc gag aac gtg gcc aag gaa tac gcc atc aca cgc gag Gly Ile Thr Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu 245 250 255			768
gcg cag gat gag ttc gcc gtc gcc tcg cag aac aag gcc gaa gcc gcg Ala Gln Asp Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala 260 265 270			816
cag aag gcc gcc aag ttt gac gaa gag atc gtc ccg gtg ctg atc ccg Gln Lys Ala Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro 275 280 285			864
cag cgc aag gcc gac ccg gtg gcc ttc aag acc gac gag ttc gtg cgc Gln Arg Lys Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg 290 295 300			912
cag gcc gcc acg ctg gac agc atg tcc gcc ctc aag ccc gcc ttc gac Gln Gly Ala Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp 305 310 315 320			960
aag gcc gcc acg gtg acc gcg gcc aac gcc tcg gcc ctg aac gac gcc Lys Ala Gly Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly 325 330 335			1008
gcc gcc gcg gtg gtg gtg atg tcg gcg gcc aag gcc aag gaa ctg gcc Ala Ala Ala Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly 340 345 350			1056
ctg acc ccg ctg gcc acg atc aag agc tat gcc aac gcc ggt gtc gat Leu Thr Pro Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp 355 360 365			1104

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ccc aag gtg atg ggc atg ggc ccg gtg ccg gcc tcc aag cgc gcc ctg 1152
 Pro Lys Val Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu
 370 375 380

tcg cgc gcc gag tgg acc ccg caa gac ctg gac ctg atg gag atc aac 1200
 Ser Arg Ala Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn
 385 390 395 400

gag gcc ttt gcc gcc cag gcg ctg gcg gtg cac cag cag atg ggc tgg 1248
 Glu Ala Phe Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp
 405 410 415

gac acc tcc aag gtc aat gtg aac ggc ggc gcc atc gcc atc ggc cac 1296
 Asp Thr Ser Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His
 420 425 430

ccg atc ggc gcg tcg ggc tgc cgt atc ctg gtg acg ctg ctg cac gag 1344
 Pro Ile Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu
 435 440 445

atg aag cgc cgt gac gcg aag aag ggc ctg gcc tcg ctg tgc atc ggc 1392
 Met Lys Arg Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly
 450 455 460

ggc gcc atg ggc gtg gcg ctg gca gtc gag cgc aaa 1428
 Gly Gly Met Gly Val Ala Leu Ala Val Glu Arg Lys
 465 470 475

<210> 11

<211> 476

<212> PRT

<213> Rastonia Eutropia

<400> 11

Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala
1 5 10 15

Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
20 25 30

Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
50 55 60

- 20 -

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
65 70 75 80

Asp Ser Arg Val Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala
85 90 95

Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu
100 105 110

Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro
115 120 125

Glu Gln Val Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser
130 135 140

Gly Gln Asn Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala
145 150 155 160

Met Val Pro Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys
165 170 175

Ala Val Met Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile
180 185 190

Val Val Ala Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu
195 200 205

Pro ~~Gly Ser~~ Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp
210 215 220

Thr Met Ile Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met
225 230 235 240

Gly Ile Thr Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu
245 250 255

Ala Gln Asp Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala
260 265 270

Gln Lys Ala Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro
275 280 285

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Gln Arg Lys Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg
 290 295 300

Gln Gly Ala Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp
 305 310 315 320

Lys Ala Gly Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly
 325 330 335

Ala Ala Ala Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly
 340 345 350

Leu Thr Pro Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp
 355 360 365

Pro Lys Val Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu
 370 375 380

Ser Arg Ala Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn
 385 390 395 400

Glu Ala Phe Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp
 405 410 415

Asp Thr Ser Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His
 420 425 430

Pro Ile Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu
 435 440 445

Met Lys Arg Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly
 450 455 460

Gly Gly Met Gly Val Ala Leu Ala Val Glu Arg Lys
 465 470 475

<210> 12

<211> 1529

<212> DNA

<213> Rastonia Eutropia

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<400> 12
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 gggggcaatc cgccgcaatg gctccattcg gcggcctcaa atccatgact ggattcccag 120
 tgaagaaggt caacactgac attacttcca ttacaagcaa tgggtggaaga gtaaagtgca 180
 tgcaggtgtg gcctccaatt ggaaagaaga agtttgagac tctttcctat ttgccaccat 240
 tgaccagaga ttcccgggtg actgacgttg tcatcgtatc cgccgcccgc accgcggtcg 300
 gcaagtttgg cggctcgctg gccaaagatcc cggcaccgga actgggtgcc gtggtcatca 360
 aggccgcgct ggagcgcgcc ggcgtcaagc cggagcaggt gagcgaagtc atcatgggcc 420
 aggtgctgac cgccggttcg ggccagaacc ccgcacgcca ggccgcgatc aaggccggcc 480
 tgccggcgat ggtgccggcc atgaccatca acaagggtgtg cggctcgggc ctgaaggccg 540
 tgatgctggc cgccaacgcg atcatggcgg gcgacgccga gatcgtggtg gccggcgggc 600
 aggaaaacat gagcgccgcc ccgcacgtgc tgccgggctc gcgcgatggt ttccgcatgg 660
 gcgatgccaa gctggtcgac accatgatcg tcgacggcct gtgggacgtg tacaaccagt 720
 accacatggg catcacgcc gagaacgtgg ccaaggaata cggcatcaca cgcgaggcgc 780
 aggatgagtt cgccgtcggc tcgcagaaca aggccgaagc cgcgcagaag gccggcaagt 840
 ttgacgaaga gatcgtcccg gtgctgatcc cgcagcgcaa gggcgacccg gtggccttca 900
 agaccgacga gttcgtgccc cagggcgcca cgctggacag catgtccggc ctcaagcccg 960
 ccttcgacaa ggccggcacg gtgaccgcgg ccaacgcctc gggcctgaac gacggcgccg 1020
 ccgcggcgcc ggtgatgtcg gcggccaagg ccaaggaact gggcctgacc ccgctggcca 1080
 cgatcaagag ctatgccaac gccggtgtcg atcccaaggt gatgggcatg ggcccgggtg 1140
 cggcctccaa gcgcgcctcg tcgcgcgccg agtggacccc gcaagacctg gacctgatgg 1200
 agatcaacga ggcctttgcc gccagggcg tggcggtgca ccagcagatg ggctgggaca 1260
 cctccaaggt caatgtgaac ggccggcgcca tcgccatcgg ccacccgatc ggcgcgtcgg 1320
 gctgccgtat cctgggtgacg ctgctgcacg agatgaagcg ccgtgacgcg aagaagggcc 1380
 tggcctcgct gtgcatcggc ggcggcatgg gcgtggcgct ggcagtcgag cgcaaataag 1440
 gaaggggttt tccggggccg cgcgcggttg gcgcggaccc ggcgacgata acgaagccaa 1500
 tcaaggagtg gacatgactc aggggtacc - 1529

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<210> 13

<211> 987

<212> DNA

<213> Rastonia Eutropia

<220>

<221> CDS

<222> (1)..(987)

<400> 13

atg gct tct atg ata tcc tct tcc gct gtg aca aca gtc agc cgt gcc	48
Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala	
1 5 10 15	
tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc	96
Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser	
20 25 30	
atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att	144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile	
35 40 45	
aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att	192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile	
50 55 60	
gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga	240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg	
65 70 75 80	
gat tcc cgg gtg act cag cgc att gcg tat gtg acc ggc ggc atg ggt	288
Asp Ser Arg Val Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly	
85 90 95	
ggt atc gga acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt	336
Gly Ile Gly Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg	
100 105 110	
gtg gtg gcc ggt tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg	384
Val Val Ala Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu	
115 120 125	
gag cag cag aag gca ctg ggc ttc gat ttc att gcc tcg gaa ggc aat	432
Glu Gln Gln Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn	
130 135 140	
gtg gct gac tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc	480
Val Ala Asp Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser	

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145	150	155	160	
gag gtc ggc gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc				528
Glu Val Gly Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg	165	170	175	
gac gtg gtg ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc				576
Asp Val Val Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile	180	185	190	
gac acc aac ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac				624
Asp Thr Asn Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp	195	200	205	
ggc atg gcc gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg				672
Gly Met Ala Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val	210	215	220	
aac ggg cag aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag				720
Asn Gly Gln Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys	225	230	235	240
gcc ggc ctg cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc				768
Ala Gly Leu His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr	245	250	255	
aag ggc gtg acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac				816
Lys Gly Val Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp	260	265	270	
atg gtc aag gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg				864
Met Val Lys Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr	275	280	285	
atc ccg gtc aag cgc ctg ggc ctg cca gaa gag atc gcc tcg atc tgc				912
Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys	290	295	300	
gcc tgg ttg tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc				960
Ala Trp Leu Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe	305	310	315	320
tcg ctc aac ggc ggc ctg cat atg ggc				987
Ser Leu Asn Gly Gly Leu His Met Gly	325			

<210> 14

<211> 329

<212> PRT

<213> Rastonia Eutropia

- 25 -

<400> 14

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Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
 20 25 30

Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
 65 70 75 80

Asp Ser Arg Val Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly
 85 90 95

Gly Ile Gly Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg
 100 105 110

Val Val Ala Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu
 115 120 125

Glu Gln Gln Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn
 130 135 140

Val Ala Asp Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser
 145 150 155 160

Glu Val Gly Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg
 165 170 175

Asp Val Val Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile
 180 185 190

Asp Thr Asn Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp
 195 200 205

Gly Met Ala Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val
 210 215 220

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Asn Gly Gln Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys
 225 230 235 240

Ala Gly Leu His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr
 245 250 255

Lys Gly Val Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp
 260 265 270

Met Val Lys Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr
 275 280 285

Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys
 290 295 300

Ala Trp Leu Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe
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Ser Leu Asn Gly Gly Leu His Met Gly
 325

<210> 15

<211> 1032

<212> DNA

<213> Rastonia Eutropia

<400> 15

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 aagaaggtca acactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcattg 180
 caggtgtggc ctccaattgg aaagaagaag tttgagactc tttcctattt gccaccattg 240
 accagagatt cccgggtgac tcagcgcatt gcgtatgtga ccggcgccat ggggtggatc 300
 ggaaccgcca tttgccagcg gctggccaag gatggctttc gtgtgggtggc cggttgccggc 360
 cccaactcgc cgcgccgca aaagtggctg gagcagcaga aggactggg cttcgatttc 420
 attgcctcgg aaggcaatgt ggctgactgg gactcgacca agaccgcatt cgacaaggtc 480
 aagtccgagg tcggcgagggt tgatgtgctg atcaacaacg ccggtatcac ccgcgacgtg 540

- 27 -

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gtgttccgca agatgacccg cgccgactgg gatgcggtga tcgacaccaa cctgacctcg      600
ctgttcaacg tcaccaagca ggtgatcgac ggcatggccg accgtggctg gggccgcatc      660
gtcaacatct cgtcggtgaa cgggcagaag ggccagttcg gccagaccaa ctactccacc      720
gccaaggccg gcctgcatgg cttcaccatg gcactggcgc aggaagtggc gaccaagggc      780
gtgaccgtca acacggtctc tccgggctat atcgccaccg acatgggtcaa ggcgatccgc      840
caggacgtgc tcgacaagat cgtcgcgacg atcccgggtca agcgccctggg cctgccagaa      900
gagatgcct cgatctgcgc ctggttgctg tcggaggagt ccggtttctc gaccggcgcc      960
gacttctcgc tcaacggcgg cctgcatatg ggctgacctg ccggcctggt tccaccagtc     1020
ggcaggggta cc                                                                1032

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<210> 16

<211> 2016

<212> DNA

<213> Rastonia Eutropia

<220>

<221> CDS

<222> (1)..(2016)

<400> 16

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atg gct tct atg ata tcc tct tcc gct gtg aca aca gtc agc cgt gcc      48
Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala
1          5          10          15

tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc      96
Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
          20          25          30

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att      144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
          35          40          45

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att      192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
          50          55          60

gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga      240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg

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- 28 -

65	70				75				80								
gat tcc cgg gtg gcg acc ggc aaa ggc gcg gca gct tcc acg cag gaa	Asp Ser Arg Val Ala Thr Gly Lys Gly Ala Ala Ala Ser Thr Gln Glu				85 90				95								288
ggc aag tcc caa cca ttc aag gtc acg ccg ggg cca ttc gat cca gcc	Gly Lys Ser Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala				100 105				110								336
aca tgg ctg gaa tgg tcc cgc cag tgg cag ggc act gaa ggc aac ggc	Thr Trp Leu Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly				115 120				125								384
cac gcg gcc gcg tcc ggc att ccg ggc ctg gat gcg ctg gca ggc gtc	His Ala Ala Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val				130 135				140								432
aag atc gcg ccg gcg cag ctg ggt gat atc cag cag cgc tac atg aag	Lys Ile Ala Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys				145 150				155 160								480
gac ttc tca gcg ctg tgg cag gcc atg gcc gag ggc aag gcc gag gcc	Asp Phe Ser Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala				165 170				175								528
acc ggt ccg ctg cac gac cgg cgc ttc gcc ggc gac gca tgg cgc acc	Thr Gly Pro Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr				180 185				190								576
aac ctc cca tat cgc ttc gct gcc gcg ttc tac ctg ctc aat gcg cgc	Asn Leu Pro Tyr Arg Phe Ala Ala Phe Tyr Leu Leu Asn Ala Arg				195 200				205								624
gcc ttg acc gag ctg gcc gat gcc gtc gag gcc gat gcc aag acc cgc	Ala Leu Thr Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg				210 215				220								672
cag cgc atc cgc ttc gcg atc tcg caa tgg gtc gat gcg atg tcg ccc	Gln Arg Ile Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro				225 230				235 240								720
gcc aac ttc ctt gcc acc aat ccc gag gcg cag cgc ctg ctg atc gag	Ala Asn Phe Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu				245 250				255								768
tcg ggc ggc gaa tcg ctg cgt gcc ggc gtg cgc aac atg atg gaa gac	Ser Gly Gly Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp				260 265				270								816
ctg aca cgc ggc aag atc tcg cag acc gac gag agc gcg ttt gag gtc	Leu Thr Arg Gly Lys Ile Ser Gln Thr Asp Glu Ser Ala Phe Glu Val				275 280				285								864
ggc cgc aat gtc gcg gtg acc gaa ggc gcc gtg gtc ttc gag aac gag	Gly Arg Asn Val Ala Val Thr Glu Gly Ala Val Val Phe Glu Asn Glu				290 295				300								912

- 29 -

tac ttc cag ctg ttg cag tac aag ccg ctg acc gac aag gtg cac gcg Tyr Phe Gln Leu Leu Gln Tyr Lys Pro Leu Thr Asp Lys Val His Ala 305 310 315 320	960
cgc ccg ctg ctg atg gtg ccg ccg tgc atc aac aag tac tac atc ctg Arg Pro Leu Leu Met Val Pro Pro Cys Ile Asn Lys Tyr Tyr Ile Leu 325 330 335	1008
gac ctg cag ccg gag agc tcg ctg gtg cgc cat gtg gtg gag cag gga Asp Leu Gln Pro Glu Ser Ser Leu Val Arg His Val Val Glu Gln Gly 340 345 350	1056
cat acg gtg ttt ctg gtg tcg tgg cgc aat ccg gac gcc agc atg gcc His Thr Val Phe Leu Val Ser Trp Arg Asn Pro Asp Ala Ser Met Ala 355 360 365	1104
ggc agc acc tgg gac gac tac atc gag cac gcg gcc atc cgc gcc atc Gly Ser Thr Trp Asp Asp Tyr Ile Glu His Ala Ala Ile Arg Ala Ile 370 375 380	1152
gaa gtc gcg cgc gac atc agc ggc cag gac aag atc aac gtg ctc ggc Glu Val Ala Arg Asp Ile Ser Gly Gln Asp Lys Ile Asn Val Leu Gly 385 390 395 400	1200
ttc tgc gtg ggc ggc acc att gtc tcg acc gcg ctg gcg gtg ctg gcc Phe Cys Val Gly Gly Thr Ile Val Ser Thr Ala Leu Ala Val Leu Ala 405 410 415	1248
gcg cgc ggc gag cac ccg gcc gcc agc gtc acg ctg ctg acc acg ctg Ala Arg Gly Glu His Pro Ala Ala Ser Val Thr Leu Leu Thr Thr Leu 420 425 430	1296
ctg gac ttt gcc gac acg ggc atc ctc gac gtc ttt gtc gac gag ggc Leu Asp Phe Ala Asp Thr Gly Ile Leu Asp Val Phe Val Asp Glu Gly 435 440 445	1344
cat gtg cag ttg cgc gag gcc acg ctg ggc ggc ggc gcc ggc gcg ccg His Val Gln Leu Arg Glu Ala Thr Leu Gly Gly Gly Ala Gly Ala Pro 450 455 460	1392
tgc gcg ctg ctg cgc ggc ctt gag ctg gcc aat acc ttc tcg ttc ttg Cys Ala Leu Leu Arg Gly Leu Glu Leu Ala Asn Thr Phe Ser Phe Leu 465 470 475 480	1440
cgc ccg aac gac ctg gtg tgg aac tac gtg gtc gac aac tac ctg aag Arg Pro Asn Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys 485 490 495	1488
ggc aac acg ccg gtg ccg ttc gac ctg ctg ttc tgg aac ggc gac gcc Gly Asn Thr Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala 500 505 510	1536
acc aac ctg ccg ggg ccg tgg tac tgc tgg tac ctg cgc cac acc tac Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr 515 520 525	1584

- 30 -

ctg cag aac gag ctc aag gta ccg ggc aag ctg acc gtg tgc ggc gtg Leu Gln Asn Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val 530 535 540	1632
ccg gtg gac ctg gcc agc atc gac gtg ccg acc tat atc tac ggc tcg Pro Val Asp Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser 545 550 555 560	1680
cgc gaa gac cat atc gtg ccg tgg acc gcg gcc tat gcc tcg acc gcg Arg Glu Asp His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala 565 570 575	1728
ctg ctg gcg aac aag ctg cgc ttc gtg ctg ggt gcg tcg ggc cat atc Leu Leu Ala Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile 580 585 590	1776
gcc ggt gtg atc aac ccg ccg gcc aag aac aag gcg agc cac tgg act Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr 595 600 605	1824
aac gat gcg ctg ccg gag tcg ccg cag caa tgg ctg gcc ggc gcc atc Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile 610 615 620	1872
gag cat cac ggc agc tgg tgg ccg gac tgg acc gca tgg ctg gcc ggg Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly 625 630 635 640	1920
cag gcc ggc gcg aaa cgc gcc gcg ccc gcc aac tat ggc aat gcg cgc Gln Ala Gly Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg 645 650 655	1968
tat cgc gca atc gaa ccc gcg cct ggg cga tac gtc aaa gcc aag gca Tyr Arg Ala Ile Glu Pro Ala Pro Gly Arg Tyr Val Lys Ala Lys Ala 660 665 670	2016

<210> ~~37~~

<211> 672

<212> PRT

<213> Rastonia Eutropia

<400> 17

Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala 1 5 10 15
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Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser 20 25 30

- 31 -

Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
 65 70 75 80

Asp Ser Arg Val Ala Thr Gly Lys Gly Ala Ala Ala Ser Thr Gln Glu
 85 90 95

Gly Lys Ser Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala
 100 105 110

Thr Trp Leu Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly
 115 120 125

His Ala Ala Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val
 130 135 140

Lys Ile Ala Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys
 145 150 155 160

Asp Phe Ser Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala
 165 170 175

Thr Gly Pro Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr
 180 185 190

Asn Leu Pro Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg
 195 200 205

Ala Leu Thr Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg
 210 215 220

Gln Arg Ile Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro
 225 230 235 240

Ala Asn Phe Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu
 245 250 255

Ser Gly Gly Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp

260

270

Arg Pro Asn Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys
485 490 495

- 33 -

Gly Asn Thr Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala
500 505 510

Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr
515 520 525

Leu Gln Asn Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val
530 535 540

Pro Val Asp Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser
545 550 555 560

Arg Glu Asp His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala
565 570 575

Leu Leu Ala Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile
580 585 590

Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr
595 600 605

Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile
610 615 620

Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly
625 630 635 640

Gln Ala Gly Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg
645 650 655

Tyr Arg Ala Ile Glu Pro Ala Pro Gly Arg Tyr Val Lys Ala Lys Ala
660 665 670

<210> 18

<211> 2049

<212> DNA

<213> Rastonia Eutropia

<400> 18

- 34 -

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 aagaagggtca aactgacat tactttccatt acaagcaatg gtggaagagt aaagtgcattg 180
 caggtgtggc ctccaattgg aaagaagaag tttgagactc tttcctatatt gccaccattg 240
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 tcgcccgcga acttccttgc caccaatccc gaggcgcagc gcctgctgat cgagtcgggc 780
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 ctgaccgtgt gcggcggtgc ggtggacctg gccagcatcg acgtgccgac ctatatctac. 1680
 ggctcgcgcg aagaccatat cgtgccgtgg accgcggcct atgcctcgac cgcgctgctg 1740

- 35 -

gcgaacaagc tgcgcttcgt gctgggtgcg tcggggccata tcgccggtgt gatcaacccg 1800
 ccggccaaga acaagcgag ccactggact aacgatgcgc tgccggagtc gccgcagcaa 1860
 tggctggccg ggcgccatcga gcatcacggc agctgggtggc cggactggac cgcattggctg 1920
 gccgggacagg ccggcgcgaa acgcgccgcg cccgccaaact atggcaatgc gcgctatcgc 1980
 gcaatcgaac ccgcgcctgg gcgatacgtc aaagccaagg catgacgctt caatcgaatt 2040
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<210> 19

<211> 1680

<212> DNA

<213> P. aeruginosa

<220>

<221> CDS

<222> (1)..(1680)

<400> 19
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 acg ~~atg~~ aac ctg aat ccg gtg atc ggc atc cgg ggc aag gac ctg ctc 96
 Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
 20 25 30
 acc tcc gcg cgc atg gtc ctg ctc cag gcg gtg cgc cag ccg ctg cac 144
 Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
 35 40 45
 agc gcc agg cac gtg gcg cat ttc agc ctg gag ctg aag aac gtc ctg 192
 Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
 50 55 60
 ctc ggc cag tcg gag cta cgc cca ggc gat gac gac cga cgc ttt tcc 240
 Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
 65 70 75 80
 gat ccg gcc tgg agc cag aat cca ctg tac aag cgc tac atg cag acc 288
 Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
 85 90 95

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tac ctg gcc tgg cgc aag gag ctg cac agc tgg atc agc cac agc gac	336
Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp	
100 105 110	
ctg tgc ccg cag gac atc agt cgt ggc cag ttc gtc atc aac ctg ctg	384
Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu	
115 120 125	
acc gag gcg atg tgc ccg acc aac agc ctg agc aac ccg gcg gcg gtc	432
Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val	
130 135 140	
aag cgc ttc ttc gag acc ggc ggc aag agc ctg ctg gac ggc ctc ggc	480
Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly	
145 150 155 160	
cac ctg gcc aag gac ctg gtg aac aac ggc ggg atg ccg agc cag gtg	528
His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val	
165 170 175	
gac atg gac gcc ttc gag gtg ggc aag aac ctg gcc acc acc gag ggc	576
Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly	
180 185 190	
gcc gtg gtg ttc cgc aac gac gtg ctg gaa ctg atc cag tac cgg ccg	624
Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro	
195 200 205	
atc acc gag tgc gtg cac gaa cgc ccg ctg ctg gtg gtg ccg ccg cag	672
Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln	
210 215 220	
atc aac aag ttc tac gtc ttc gac ctg tgc ccg gac aag agc ctg gcg	720
Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala	
225 230 235 240	
cgc ttc tgc ctg cgc aac ggc gtg cag acc ttc atc gtc agt tgg cgc	768
Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg	
245 250 255	
aac ccg acc aag tgc cag cgc gaa tgg ggc ctg acc acc tat atc gag	816
Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu	
260 265 270	
gcg ctc aag gag gcc atc gag gta gtc ctg tgc atc acc ggc agc aag	864
Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys	
275 280 285	
gac ctc aac ctc ctc ggc gcc tgc tcc ggc ggg atc acc acc gcg acc	912
Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr	
290 295 300	
ctg gtc ggc cac tac gtg gcc agc ggc gag aag aag gtc aac gcc ttc	960
Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe	
305 310 315 320	
acc caa ctg gtc agc gtg ctc gac ttc gaa ctg aat acc cag gtc gcg	1008

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Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala	325	330	335	
ctg ttc gcc gac gag aag act ctg gag gcc gcc aag cgt cgt tcc tac				1056
Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr	340	345	350	
cag tcc gcc gtg ctg gag ggc aag gac atg gcc aag gtg ttc gcc tgg				1104
Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp	355	360	365	
atg cgc ccc aac gac ctg atc tgg aac tac tgg gtc aac aac tac ctg				1152
Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu	370	375	380	
ctc gcc aac cag ccg ccg gcg ttc gac atc ctc tac tgg aac aac gac				1200
Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp	385	390	395	400
acc acg cgc ctg ccc gcc gcg ctg cac ggc gag ttc gtc gaa ctg ttc				1248
Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe	405	410	415	
aag agc aac ccg ctg aac cgc ccc ggc gcc ctg gag gtc tcc gcc acg				1296
Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr	420	425	430	
ccc atc gac ctg aag cag gtg act tgc gac ttc tac tgt gtc gcc ggt				1344
Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly	435	440	445	
ctg aac gac cac atc acc ccc tgg gag tcg tgc tac aag tcg gcc agg				1392
Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg	450	455	460	
ctg ctg ggt gcc aag tgc gag ttc atc ctc tcc aac agc ggt cac atc				1440
Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile	465	470	475	480
cag agc atc ctc aac cca ccg ggc aac ccc aag gca cgc ttc atg acc				1488
Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr	485	490	495	
aat ccg gaa ctg ccc gcc gag ccc aag gcc tgg ctg gaa cag gcc gcc				1536
Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly	500	505	510	
aag cac gcc gac tcg tgg tgg ttg cac tgg cag caa tgg ctg gcc gaa				1584
Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu	515	520	525	
cgc tcc gcc aag acc cgc aag gcg ccc gcc agc ctg gcc aac aag acc				1632
Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr	530	535	540	
tat ccg gcc gcc gaa gcc gcg ccc gga acc tac gtg cat gaa cga tga				1680
Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg				

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545

550

555

<210> 20

<211> 559

<212> PRT

<213> P. aeruginosa

<400> 20

Met Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala Ala Glu Asn
 1 5 10 15

Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
 20 25 30

Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
 35 40 45

Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
 50 55 60

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
 65 70 75 80

Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
 85 90 95

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp
 100 105 110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu
 115 120 125

Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val
 130 135 140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly
 145 150 155 160

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val
 165 170 175

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Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly
 180 185 190

Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro
 195 200 205

Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln
 210 215 220

Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala
 225 230 235 240

Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg
 245 250 255

Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu
 260 265 270

Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys
 275 280 285

Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr
 290 295 300

Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe
 305 310 315 320

Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala
 325 330 335

Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr
 340 345 350

Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp
 355 360 365

Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu
 370 375 380

Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp
 385 390 395 400

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Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe
 405 410 415

Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr
 420 425 430

Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly
 435 440 445

Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg
 450 455 460

Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile
 465 470 475 480

Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr
 485 490 495

Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly
 500 505 510

Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu
 515 520 525

Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr
 530 535 540

Tyr ~~Pro~~ Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg
 545 550 555

<210> 21

<211> 1692

<212> DNA

<213> P. aeruginosa

<400> 21

ggatccatga gtcagaagaa caataacgag cttcccaagc aagccgcgga aaacacgctg 60

aacctgaatc cgggtgatcgg catccggggc aaggacctgc tcacctccgc gcgcatggtc 120

ctgctccagg cgggtgcgcca gccgctgcac agcgccaggc acgtggcgca tttcagcctg 180

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gagctgaaga acgtcctgct cggccagtcg gagctacgcc caggcgatga cgaccgacgc 240
 ttttccgatc cggcctggag ccagaatcca ctgtacaagc gctacatgca gacctacctg 300
 gcctggcgca aggagctgca cagctggatc agccacagcg acctgtcgcc gcaggacatc 360
 agtcgtggcc agttcgtcat caacctgctg accgaggcga tgtcgccgac caacagcctg 420
 agcaaccctg cggcggtcaa gcgcttcttc gagaccggcg gcaagagcct gctggacggc 480
 ctcggccacc tggccaagga cctggtgaac aacggcggga tgccgagcca ggtggacatg 540
 gacgccttcg aggtgggcaa gaacctggcc accaccgagg gcgccgtggt gttccgcaac 600
 gacgtgctgg aactgatcca gtacgggocg atcaccgagt cgggtgcacga acgcccgtg 660
 ctggtggtgc cgccgcagat caacaagttc tacgtcttcg acctgtcgcc ggacaagagc 720
 ctggcgcgct tctgcctgcg caacggcgtg cagaccttca tcgtcagttg gcgcaaccgc 780
 accaagtcgc agcgcgaaatg gggcctgacc acctatatcg aggcgtcaa ggaggccatc 840
 gaggtagtcc tgtcgatcac cggcagcaag gacctcaacc tcctcggcgc ctgctccggc 900
 gggatcacca ccgcgaccct ggtcgccac tacgtggcca gcggcgagaa gaaggtcaac 960
 gccttcaccc aactggtcag cgtgctogac ttcgaaactga ataccaggt cgcgctgttc 1020
 gccgacgaga agactctgga ggccgccaag cgtcgttcct accagtccgg cgtgctggag 1080
 ggcaaggaca tggccaaggt gttcgcttg atgcgcccc aacgacctgat ctggaactac 1140
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 aacgacacca cgcgcctgcc cgccgcgctg cacggcgagt tcgtcgaact gttcaagagc 1260
 aacccgctga accgccccgc cgccctggag gtctccggca cggccatcga cctgaagcag 1320
 gtgacttgcg acttctactg tgtcgccggt ctgaacgacc acatcacccc ctgggagtcg 1380
 tgctacaagt cggccaggct gctgggtggc aagtgcgagt tcacctctc caacagcggc 1440
 cacatccaga gcacctcaa cccaccgggc aaccccaagg cacgcttcat gaccaatccg 1500
 gaactgccc cagagcccaa ggccctggctg gaacaggccg gcaagcacgc cgactcgtgg 1560
 tggttgcact ggcagcaatg gctggccgaa cgctccggca agaccgcaa ggcgcccgcc 1620
 agcctgggca acaagaccta tccggccggc gaagccgcgc ccggaaccta cgtgcatgaa 1680
 cgatgaggta cc 1692

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<211> 1794

<212> DNA

<213> P. aeruginosa

<220>

<221> CDS

<222> (1)..(1794)

<400> 22

atg agt cag aag aac aat aac gag ctt ccc aag caa gcc gcg gaa aac	48
Met Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala Ala Glu Asn	
1 5 10 15	
acg ctg aac ctg aat ccg gtg atc ggc atc cgg ggc aag gac ctg ctc	96
Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu	
20 25 30	
acc tcc gcg cgc atg gtc ctg ctc cag gcg gtg cgc cag ccg ctg cac	144
Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His	
35 40 45	
agc gcc agg cac gtg gcg cat ttc agc ctg gag ctg aag aac gtc ctg	192
Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu	
50 55 60	
ctc ggc cag tcg gag cta cgc cca ggc gat gac gac cga cgc ttt tcc	240
Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser	
65 70 75 80	
gat ccg gcc tgg agc cag aat cca ctg tac aag cgc tac atg cag acc	288
Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr	
85 90 95	
tac ctg gcc tgg cgc aag gag ctg cac agc tgg atc agc cac agc gac	336
Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp	
100 105 110	
ctg tcg ccg cag gac atc agt cgt ggc cag ttc gtc atc aac ctg ctg	384
Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu	
115 120 125	
acc gag gcg atg tcg ccg acc aac agc ctg agc aac ccg gcg gcg gtc	432
Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val	
130 135 140	
aag cgc ttc ttc gag acc ggc ggc aag agc ctg ctg gac ggc ctc ggc	480
Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly	
145 150 155 160	

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cac ctg gcc aag gac ctg gtg aac aac ggc ggg atg ccg agc cag gtg His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val 165 170 175	528
gac atg gac gcc ttc gag gtg ggc aag aac ctg gcc acc acc gag ggc Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly 180 185 190	576
gcc gtg gtg ttc cgc aac gac gtg ctg gaa ctg atc cag tac cgg ccg Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro 195 200 205	624
atc acc gag tcg gtg cac gaa cgc ccg ctg ctg gtg gtg ccg ccg cag Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln 210 215 220	672
atc aac aag ttc tac gtc ttc gac ctg tcg ccg gac aag agc ctg gcg Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala 225 230 235 240	720
cgc ttc tgc ctg cgc aac ggc gtg cag acc ttc atc gtc agt tgg cgc Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg 245 250 255	768
aac ccg acc aag tcg cag cgc gaa tgg ggc ctg acc acc tat atc gag Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu 260 265 270	816
gcg ctc aag gag gcc atc gag gta gtc ctg tcg atc acc ggc agc aag Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys 275 280 285	864
gac ctc aac ctc ctc ggc gcc tgc tcc ggc ggg atc acc acc gcg acc Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr 290 295 300	912
ctg gtc ggc cac tac gtg gcc agc ggc gag aag aag gtc aac gcc ttc Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe 305 310 315 320	960
acc caa ctg gtc agc gtg ctc gac ttc gaa ctg aat acc cag gtc gcg Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala 325 330 335	1008
ctg ttc gcc gac gag aag act ctg gag gcc gcc aag cgt cgt tcc tac Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr 340 345 350	1056
cag tcc ggc gtg ctg gag ggc aag gac atg gcc aag gtg ttc gcc tgg Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp 355 360 365	1104
atg cgc ccc aac gac ctg atc tgg aac tac tgg gtc aac aac tac ctg Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu 370 375 380	1152
ctc ggc aac cag ccg ccg gcg ttc gac atc ctc tac tgg aac aac gac	1200

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Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp	
385 390 395 400	
acc acg cgc ctg ccc gcc gcg ctg cac ggc gag ttc gtc gaa ctg ttc	1248
Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe	
405 410 415	
aag agc aac ccg ctg aac cgc ccc ggc gcc ctg gag gtc tcc ggc acg	1296
Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr	
420 425 430	
ccc atc gac ctg aag cag gtg act tgc gac ttc tac tgt gtc gcc ggt	1344
Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly	
435 440 445	
ctg aac gac cac atc acc ccc tgg gag tcg tgc tac aag tcg gcc agg	1392
Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg	
450 455 460	
ctg ctg ggt ggc aag tgc gag ttc atc ctc tcc aac agc ggt cac atc	1440
Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile	
465 470 475 480	
cag agc atc ctc aac cca ccg ggc aac ccc aag gca cgc ttc atg acc	1488
Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr	
485 490 495	
aat ccg gaa ctg ccc gcc gag ccc aag gcc tgg ctg gaa cag gcc ggc	1536
Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly	
500 505 510	
aag cac gcc gac tcg tgg tgg ttg cac tgg cag caa tgg ctg gcc gaa	1584
Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu	
515 520 525	
cgc tcc ggc aag acc cgc aag gcg ccc gcc agc ctg ggc aac aag acc	1632
Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr	
<u>530</u> 535 540	
tat ccg gcc ggc gaa gcc gcg ccc gga acc tac gtg cat gaa cga tca	1680
Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg Ser	
545 550 555 560	
aaa gct ttg ggc aaa ggt gtt acc gag gaa caa ttc aaa gag acc tgg	1728
Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp	
565 570 575	
acg agg ccg gga gct gct gga atg ggc gaa ggg act agc ott gtg gtg	1776
Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val	
580 585 590	
gcc aag tcc aga atg taa	1794
Ala Lys Ser Arg Met	
595	

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<210> 23

<211> 597

<212> PRT

<213> P. aeruginosa

<400> 23

Met Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala Ala Glu Asn
 1 5 10 15

Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
 20 25 30

Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
 35 40 45

Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
 50 55 60

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
 65 70 75 80

Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
 85 90 95

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp
 100 105 110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu
 115 120 125

Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val
 130 135 140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly
 145 150 155 160

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val
 165 170 175

Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly

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180	185	190
Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro		
195	200	205
Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln		
210	215	220
Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala		
225	230	235
Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg		
245	250	255
Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu		
260	265	270
Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys		
275	280	285
Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr		
290	295	300
Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe		
305	310	315
Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala		
325	330	335
Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr		
340	345	350
Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp		
355	360	365
Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu		
370	375	380
Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp		
385	390	395
Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe		
405	410	415

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Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr
 420 425 430

Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly
 435 440 445

Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg
 450 455 460

Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile
 465 470 475 480

Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr
 485 490 495

Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly
 500 505 510

Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu
 515 520 525

Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr
 530 535 540

Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg Ser
 545 550 555 560

Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp
 565 570 575

Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val
 580 585 590

Ala Lys Ser Arg Met
 595

<210> 24

<211> 1883

<212> DNA

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<213> P. aeruginosa

<400> 24

ggatcccca	ttcccgatga	gtcagaagaa	caataacgag	cttcccaagc	aagccgcgga	60
aaacacgctg	aacctgaatc	cggtgatcgg	catccggggc	aaggacctgc	tcacctccgc	120
gcgcatggtc	ctgctccagg	cggtgcgcca	gccgctgcac	agcgccaggc	acgtggcgca	180
tttcagcctg	gagctgaaga	acgtcctgct	cggccagtcg	gagctacgcc	caggcgatga	240
cgaccgacgc	ttttccgatc	cggcctggag	ccagaatcca	ctgtacaagc	gctacatgca	300
gacctacctg	gcctggcgca	aggagctgca	cagctggatc	agccacagcg	acctgtcgcc	360
gcaggacatc	agtcgtggcc	agttcgatcat	caacctgctg	accgaggcga	tgtcgccgac	420
caacagcctg	agcaaccg	cggcgggtcaa	gcgcttcttc	gagaccggcg	gcaagagcct	480
gctggacggc	ctcgccacc	tggccaagga	cctggtgaac	aacggcgga	tgccgagcca	540
ggtggacatg	gacgccttcg	aggtgggcaa	gaacctggcc	accaccgagg	gcgcggtggt	600
gttccgcaac	gacgtgctgg	aactgatcca	gtaccggccg	atcaccgagt	cggtgcacga	660
acgcccgtg	ctggtggtgc	cgccgcagat	caacaagttc	tacgtcttcg	acctgtcgcc	720
ggacaagagc	ctggcgcgct	tctgcctg	caacggcgctg	cagaccttca	togtcagttg	780
gcgcaaccg	accaagtgc	agcgogaatg	gggcctgacc	acctatatcg	aggcgctcaa	840
ggaggccatc	gaggtagtcc	tgtcgatcac	cggcagcaag	gacctcaacc	tcctcggcgc	900
ctgctccggc	gggatcacca	ccgcgaccct	ggtcggccac	tacgtggcca	gcggcgagaa	960
gaaggtcacc	gccttcaccc	aactggtcag	cgtgctcgac	ttcgaactga	atacccaggt	1020
cgcgctgttc	gccgacgaga	agactctgga	ggccgccaag	cgtcgttcct	accagtccgg	1080
cgtgctggag	ggcaaggaca	tggccaaggt	gttcgcctgg	atgcgcccc	acgacctgat	1140
ctggaactac	tgggtcaaca	actacctgct	cggcaaccag	ccgcggcggt	tgcacatcct	1200
ctactggaac	aacgacacca	cgcgccctgcc	cgccgcgctg	cacggcgagt	togtcgaact	1260
gttcaagagc	aaccgcgtga	accgccccgg	cggcctggag	gtctccggca	cggccatcga	1320
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ctgggagtcg	tgtacaagt	cggccaggct	gctgggtggc	aagtgcgagt	tcactctctc	1440
caacagcggt	cacatccaga	gcacccctcaa	cccaccgggc	aaccccaagg	cacgcttcat	1500
gaccaatccg	gaactgccc	ccgagcccaa	ggcctgggtg	gaacaggccg	gcaagcacgc	1560

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cgactcgtgg tggttgcact ggcagcaatg gctggccgaa cgctccggca agacccgcaa 1620
 ggcgcccgcc agcctgggca acaagaccta tccggccggc gaagccgccc ccggaaccta 1680
 cgtgcatgaa cgatcaaaag ctttgggcaa aggtgttacc gaggaacaat tcaaagagac 1740
 ctggacgagg ccgggagctg ctggaatggg cgaagggcga agggactagc cttgtggtgg 1800
 ccaagtccag aatgtaagac agacgttcat tgccggcggag cggccaaggc ggttcggcat 1860
 cttcgcagaa aaacaactag ggg 1883

<210> 25

<211> 1929

<212> DNA

<213> *P. aeruginosa*

<220>

<221> CDS

<222> (1)..(1929)

<400> 25

atg gct tct atg ata tcc tct tcc gct gtg aca aca gtc agc cgt gcc 48
 Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala
 1 5 10 15

tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc 96
 Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
 20 25 30

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att 144
 Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
 35 40 45

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att 192
 Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
 50 55 60

gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga 240
 Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
 65 70 75 80

gat tcc cgg gtg agt cag aag aac aat aac gag ctt ccc aag caa gcc 288
 Asp Ser Arg Val Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala
 85 90 95

gcg gaa aac acg ctg aac ctg aat ccg gtg atc ggc atc cgg ggc aag 336

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Ala	Glu	Asn	Thr	Leu	Asn	Leu	Asn	Pro	Val	Ile	Gly	Ile	Arg	Gly	Lys	
			100					105					110			
gac	ctg	ctc	acc	tcc	gcg	cgc	atg	gtc	ctg	ctc	cag	gcg	gtg	cgc	cag	384
Asp	Leu	Leu	Thr	Ser	Ala	Arg	Met	Val	Leu	Leu	Gln	Ala	Val	Arg	Gln	
		115					120					125				
ccg	ctg	cac	agc	gcc	agg	cac	gtg	gcg	cat	ttc	agc	ctg	gag	ctg	aag	432
Pro	Leu	His	Ser	Ala	Arg	His	Val	Ala	His	Phe	Ser	Leu	Glu	Leu	Lys	
	130					135					140					
aac	gtc	ctg	ctc	ggc	cag	tcg	gag	cta	cgc	cca	ggc	gat	gac	gac	cga	480
Asn	Val	Leu	Leu	Gly	Gln	Ser	Glu	Leu	Arg	Pro	Gly	Asp	Asp	Asp	Arg	
145					150					155					160	
cgc	ttt	tcc	gat	ccg	gcc	tgg	agc	cag	aat	cca	ctg	tac	aag	cgc	tac	528
Arg	Phe	Ser	Asp	Pro	Ala	Trp	Ser	Gln	Asn	Pro	Leu	Tyr	Lys	Arg	Tyr	
				165					170					175		
atg	cag	acc	tac	ctg	gcc	tgg	cgc	aag	gag	ctg	cac	agc	tgg	atc	agc	576
Met	Gln	Thr	Tyr	Leu	Ala	Trp	Arg	Lys	Glu	Leu	His	Ser	Trp	Ile	Ser	
			180					185					190			
cac	agc	gac	ctg	tcg	ccg	cag	gac	atc	agt	cgt	ggc	cag	ttc	gtc	atc	624
His	Ser	Asp	Leu	Ser	Pro	Gln	Asp	Ile	Ser	Arg	Gly	Gln	Phe	Val	Ile	
		195					200					205				
aac	ctg	ctg	acc	gag	gcg	atg	tcg	ccg	acc	aac	agc	ctg	agc	aac	ccg	672
Asn	Leu	Leu	Thr	Glu	Ala	Met	Ser	Pro	Thr	Asn	Ser	Leu	Ser	Asn	Pro	
	210					215					220					
gcg	gcg	gtc	aag	cgc	ttc	ttc	gag	acc	ggc	ggc	aag	agc	ctg	ctg	gac	720
Ala	Ala	Val	Lys	Arg	Phe	Phe	Glu	Thr	Gly	Gly	Lys	Ser	Leu	Leu	Asp	
225					230					235					240	
ggc	ctc	ggc	cac	ctg	gcc	aag	gac	ctg	gtg	aac	aac	ggc	ggg	atg	ccg	768
Gly	Leu	Gly	His	Leu	Ala	Lys	Asp	Leu	Val	Asn	Asn	Gly	Gly	Met	Pro	
				245					250					255		
agc	cag	gtg	gac	atg	gac	gcc	ttc	gag	gtg	ggc	aag	aac	ctg	gcc	acc	816
Ser	Gln	Val	Asp	Met	Asp	Ala	Phe	Glu	Val	Gly	Lys	Asn	Leu	Ala	Thr	
			260					265					270			
acc	gag	ggc	gcc	gtg	gtg	ttc	cgc	aac	gac	gtg	ctg	gaa	ctg	atc	cag	864
Thr	Glu	Gly	Ala	Val	Val	Phe	Arg	Asn	Asp	Val	Leu	Glu	Leu	Ile	Gln	
		275					280					285				
tac	cgg	ccg	atc	acc	gag	tcg	gtg	cac	gaa	cgc	ccg	ctg	ctg	gtg	gtg	912
Tyr	Arg	Pro	Ile	Thr	Glu	Ser	Val	His	Glu	Arg	Pro	Leu	Leu	Val	Val	
	290					295					300					
ccg	ccg	cag	atc	aac	aag	ttc	tac	gtc	ttc	gac	ctg	tcg	ccg	gac	aag	960
Pro	Pro	Gln	Ile	Asn	Lys	Phe	Tyr	Val	Phe	Asp	Leu	Ser	Pro	Asp	Lys	
305					310					315					320	
agc	ctg	gcg	cgc	ttc	tgc	ctg	cgc	aac	ggc	gtg	cag	acc	ttc	atc	gtc	1008
Ser	Leu	Ala	Arg	Phe	Cys	Leu	Arg	Asn	Gly	Val	Gln	Thr	Phe	Ile	Val	

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325										330					335					
agt	tgg	cgc	aac	ccg	acc	aag	tcg	cag	cgc	gaa	tgg	ggc	ctg	acc	acc					1056
Ser	Trp	Arg	Asn	Pro	Thr	Lys	Ser	Gln	Arg	Glu	Trp	Gly	Leu	Thr	Thr					
			340					345					350							
tat	atc	gag	gcg	ctc	aag	gag	gcc	atc	gag	gta	gtc	ctg	tcg	atc	acc					1104
Tyr	Ile	Glu	Ala	Leu	Lys	Glu	Ala	Ile	Glu	Val	Val	Leu	Ser	Ile	Thr					
		355					360					365								
ggc	agc	aag	gac	ctc	aac	ctc	ctc	ggc	gcc	tgc	tcc	ggc	ggg	atc	acc					1152
Gly	Ser	Lys	Asp	Leu	Asn	Leu	Leu	Gly	Ala	Cys	Ser	Gly	Gly	Ile	Thr					
	370					375					380									
acc	gcg	acc	ctg	gtc	ggc	cac	tac	gtg	gcc	agc	ggc	gag	aag	aag	gtc					1200
Thr	Ala	Thr	Leu	Val	Gly	His	Tyr	Val	Ala	Ser	Gly	Glu	Lys	Lys	Val					
385					390				395						400					
aac	gcc	ttc	acc	caa	ctg	gtc	agc	gtg	ctc	gac	ttc	gaa	ctg	aat	acc					1248
Asn	Ala	Phe	Thr	Gln	Leu	Val	Ser	Val	Leu	Asp	Phe	Glu	Leu	Asn	Thr					
			405					410						415						
cag	gtc	gcg	ctg	ttc	gcc	gac	gag	aag	act	ctg	gag	gcc	gcc	aag	cgt					1296
Gln	Val	Ala	Leu	Phe	Ala	Asp	Glu	Lys	Thr	Leu	Glu	Ala	Ala	Lys	Arg					
			420				425						430							
cgt	tcc	tac	cag	tcc	ggc	gtg	ctg	gag	ggc	aag	gac	atg	gcc	aag	gtg					1344
Arg	Ser	Tyr	Gln	Ser	Gly	Val	Leu	Glu	Gly	Lys	Asp	Met	Ala	Lys	Val					
		435				440						445								
ttc	gcc	tgg	atg	cgc	ccc	aac	gac	ctg	atc	tgg	aac	tac	tgg	gtc	aac					1392
Phe	Ala	Trp	Met	Arg	Pro	Asn	Asp	Leu	Ile	Trp	Asn	Tyr	Trp	Val	Asn					
	450					455					460									
aac	tac	ctg	ctc	ggc	aac	cag	ccg	ccg	gcg	ttc	gac	atc	ctc	tac	tgg					1440
Asn	Tyr	Leu	Leu	Gly	Asn	Gln	Pro	Pro	Ala	Phe	Asp	Ile	Leu	Tyr	Trp					
465				470					475					480						
aac	aac	gac	acc	acg	cgc	ctg	ccc	gcc	gcg	ctg	cac	ggc	gag	ttc	gtc					1488
Asn	Asn	Asp	Thr	Thr	Arg	Leu	Pro	Ala	Ala	Leu	His	Gly	Glu	Phe	Val					
			485					490					495							
gaa	ctg	ttc	aag	agc	aac	ccg	ctg	aac	cgc	ccc	ggc	gcc	ctg	gag	gtc					1536
Glu	Leu	Phe	Lys	Ser	Asn	Pro	Leu	Asn	Arg	Pro	Gly	Ala	Leu	Glu	Val					
			500				505						510							
tcc	ggc	acg	ccc	atc	gac	ctg	aag	cag	gtg	act	tgc	gac	ttc	tac	tgt					1584
Ser	Gly	Thr	Pro	Ile	Asp	Leu	Lys	Gln	Val	Thr	Cys	Asp	Phe	Tyr	Cys					
		515				520						525								
gtc	gcc	ggg	ctg	aac	gac	cac	atc	acc	ccc	tgg	gag	tcg	tgc	tac	aag					1632
Val	Ala	Gly	Leu	Asn	Asp	His	Ile	Thr	Pro	Trp	Glu	Ser	Cys	Tyr	Lys					
	530				535					540										
tcg	gcc	agg	ctg	ctg	ggg	ggc	aag	tgc	gag	ttc	atc	ctc	tcc	aac	agc					1680
Ser	Ala	Arg	Leu	Leu	Gly	Gly	Lys	Cys	Glu	Phe	Ile	Leu	Ser	Asn	Ser					
545					550				555						560					

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ggt cac atc cag agc atc ctc aac cca ccg ggc aac ccc aag gca cgc	1728
Gly His Ile Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg	
565 570 575	
ttc atg acc aat ccg gaa ctg ccc gcc gag ccc aag gcc tgg ctg gaa	1776
Phe Met Thr Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu	
580 585 590	
cag gcc ggc aag cac gcc gac tcg tgg tgg ttg cac tgg cag caa tgg	1824
Gln Ala Gly Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp	
595 600 605	
ctg gcc gaa cgc tcc ggc aag acc cgc aag gcg ccc gcc agc ctg gcc	1872
Leu Ala Glu Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly	
610 615 620	
aac aag acc tat ccg gcc ggc gaa gcc gcg ccc gga acc tac gtg cat	1920
Asn Lys Thr Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His	
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gaa cga tga	1929
Glu Arg	

<210> 26

<211> 642

<212> PRT

<213> P. aeruginosa

<400> 26

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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
65 70 75 80

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Asp Ser Arg Val Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala
85 90 95

Ala Glu Asn Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys
100 105 110

Asp Leu Leu Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln
115 120 125

Pro Leu His Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys
130 135 140

Asn Val Leu Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg
145 150 155 160

Arg Phe Ser Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr
165 170 175

Met Gln Thr Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser
180 185 190

His Ser Asp Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile
195 200 205

Asn Leu Leu Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro
210 215 220

Ala ~~Ala Val~~ Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp
225 230 235 240

Gly Leu Gly His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro
245 250 255

Ser Gln Val Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr
260 265 270

Thr Glu Gly Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln
275 280 285

Tyr Arg Pro Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val
290 295 300

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Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys
305 310 315 320

Ser Leu Ala Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val
325 330 335

Ser Trp Arg Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr
340 345 350

Tyr Ile Glu Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr
355 360 365

Gly Ser Lys Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr
370 375 380

Thr Ala Thr Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val
385 390 395 400

Asn Ala Phe Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr
405 410 415

Gln Val Ala Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg
420 425 430

Arg Ser Tyr Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val
435 440 445

Phe Ala Trp Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn
~~450~~ 455 460

Asn Tyr Leu Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp
465 470 475 480

Asn Asn Asp Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val
485 490 495

Glu Leu Phe Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val
500 505 510

Ser Gly Thr Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys
515 520 525

Val Ala Gly Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys

- 55 -

530 535 540
 Ser Ala Arg Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser
 545 550 555 560
 Gly His Ile Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg
 565 570 575
 Phe Met Thr Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu
 580 585 590
 Gln Ala Gly Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp
 595 600 605
 Leu Ala Glu Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly
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 Asn Lys Thr Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His
 625 630 635 640
 Glu Arg

<210> 27

<211> 1941

<212> DNA

<213> ~~B.~~ aeruginosa

<400> 27

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 aagaaggtca aactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcag 180
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 ttcagcctgg agctgaagaa cgtcctgctc ggccagtcgg agctacgccc aggcgatgac 480

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<210> 28

<211> 1137

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<212> DNA

<213> *Pseudomonas putida*

<220>

<221> CDS

<222> (1)..(1137)

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tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc      96
Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
          20          25          30

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att      144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
          35          40          45

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att      192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
          50          55          60

gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga      240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
65          70          75          80

gat tcc cgg gtg agg cca gaa atc gct gta ctt gat atc caa ggt cag      288
Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln
          85          90          95

tat cgg gtt tac acg gag ttc tat cgc gcg gat gcg gcc gaa aac acg      336
Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr
          100          105          110

atc atc ctg atc aac ggc tcg ctg gcc acc acg gcc tcg ttc gcc cag      384
Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln
          115          120          125

acg gta cgt aac ctg cac cca cag ttc aac gtg gtt ctg ttc gac cag      432
Thr Val Arg Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln
          130          135          140

ccg tat tca ggc aag tcc aag ccg cac aac cgt cag gaa cgg ctg atc      480
Pro Tyr Ser Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile
          145          150          155          160

agc aag gag acc gag gcg cat atc ctc ctt gag ctg atc gag cac ttc      528
Ser Lys Glu Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe

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	165	170	175	
cag gca gac cac gtg atg tct ttt tcg tgg ggt ggc gca agc acg ctg				576
Gln Ala Asp His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu				
	180	185	190	
ctg gcg ctg gcg cac cag ccg cgg tac gtg aag aag gca gtg gtg agt				624
Leu Ala Leu Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser				
	195	200	205	
tcg ttc tcg cca gtg atc aac gag ccg atg cgc gac tat ctg gac cgt				672
Ser Phe Ser Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg				
	210	215	220	
ggc tgc cag tac ctg gcc gcc tgc gac cgt tat cag gtc ggc aac ctg				720
Gly Cys Gln Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu				
	225	230	235	240
gtc aat gac acc atc ggc aag cac ttg ccg tcg ctg ttc aaa cgc ttc				768
Val Asn Asp Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe				
	245	250	255	
aac tac cgc cat gtg agc agc ctg gac agc cac gag tac gca cag atg				816
Asn Tyr Arg His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met				
	260	265	270	
cac ttc cac atc aac cag gtg ctg gag cac gac ctg gaa cgt gcg ctg				864
His Phe His Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu				
	275	280	285	
caa ggc gcg cgc aat atc aac atc ccg gtg ctg ttc atc aac ggc gag				912
Gln Gly Ala Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu				
	290	295	300	
cgc gac gag tac acc aca gtc gag gat gcg cgg cag ttc agc aag cat				960
Arg Asp Glu Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His				
	305	310	315	320
gtg ggc aga agc cag ttc agc gtg atc cgc gat gcg ggc cac ttc ctg				1008
Val Gly Arg Ser Gln Phe Ser Val Ile Arg Asp Ala Gly His Phe Leu				
	325	330	335	
gac atg gag aac aag acc gcc tgc gag aac acc cgc aat gtc atg ctg				1056
Asp Met Glu Asn Lys Thr Ala Cys Glu Asn Thr Arg Asn Val Met Leu				
	340	345	350	
ggc ttc ctc aag cca acc gtg cgt gaa ccc cgc caa cgt tac caa ccc				1104
Gly Phe Leu Lys Pro Thr Val Arg Glu Pro Arg Gln Arg Tyr Gln Pro				
	355	360	365	
gtg cag cag ggg cag cat gca ttt gcc atc tga				1137
Val Gln Gln Gly Gln His Ala Phe Ala Ile				
	370	375		

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<211> 378

<212> PRT

<213> Pseudomonas putida

<400> 29

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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
 65 70 75 80

Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln
 85 90 95

Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr
 100 105 110

Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln
 115 120 125

Thr Val Arg Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln
 130 135 140

Pro Tyr Ser Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile
 145 150 155 160

Ser Lys Glu Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe
 165 170 175

Gln Ala Asp His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu
 180 185 190

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Leu Ala Leu Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser
 195 200 205

Ser Phe Ser Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg
 210 215 220

Gly Cys Gln Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu
 225 230 235 240

Val Asn Asp Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe
 245 250 255

Asn Tyr Arg His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met
 260 265 270

His Phe His Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu
 275 280 285

Gln Gly Ala Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu
 290 295 300

Arg Asp Glu Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His
 305 310 315 320

Val Gly Arg Ser Gln Phe Ser Val Ile Arg Asp Ala Gly His Phe Leu
 325 330 335

Asp ~~Met~~ Glu Asn Lys Thr Ala Cys Glu Asn Thr Arg Asn Val Met Leu
 340 345 350

Gly Phe Leu Lys Pro Thr Val Arg Glu Pro Arg Gln Arg Tyr Gln Pro
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Val Gln Gln Gly Gln His Ala Phe Ala Ile
 370 375

<210> 30

<211> 1149

<212> DNA

<213> Pseudomonas putida

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 aagaaggatca aactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcattg 180
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 aacctggtca atgacaccat cggcaagcac ttgccgtcgc tgttcaaacg cttcaactac 780
 cgccatgtga gcagcctgga cagccacgag tacgcacaga tgcacttcca catcaaccag 840
 gtgctggagc acgacctgga acgtgcgctg caaggcgcg ccaatatcaa catcccgggtg 900
 ctgttcatca acggcgagcg cgacgagtac accacagtcg aggatgcgcg gcagttcagc 960
 aagcatgtgg gcagaagcca gttcagcgtg atccgcgatg cgggccactt cctggacatg 1020
 gagaaacagg ccgcctgcga gaacacccgc aatgtcatgc tgggcttcct caagccaacc 1080
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<210> 31

<211> 519

<212> DNA

<213> *Aeromonas caviae*

<220>

- 62 -

<221> CDS

<222> (1)..(519)

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<400> 31
atg agc gca caa tcc ctg gaa gta ggc cag aag gcc cgt ctc agc aag      48
Met Ser Ala Gln Ser Leu Glu Val Gly Gln Lys Ala Arg Leu Ser Lys
1          5          10          15

cgg ttc ggg gcg gcg gag gta gcc gcc ttc gcc gcg ctc tcg gag gac      96
Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser Glu Asp
          20          25          30

ttc aac ccc ctg cac ctg gac ccg gcc ttc gcc gcc acc acg gcg ttc      144
Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe
          35          40          45

gag cgg ccc ata gtc cac ggc atg ctg ctc gcc agc ctc ttc tcc ggg      192
Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly
          50          55          60

ctg ctg ggc cag cag ttg ccg ggc aag ggg agc atc tat ctg ggt caa      240
Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gln
65          70          75          80

agc ctc agc ttc aag ctg ccg gtc ttt gtc ggg gac gag gtg acg gcc      288
Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala
          85          90          95

gag gtg gag gtg acc gcc ctt cgc gag gac aag ccc atc gcc acc ctg      336
Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu
          100          105          110

acc acc cgc atc ttc acc caa ggc ggc gcc ctc gcc gtg acg ggg gaa      384
Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu
          115          120          125

gcc gtg gtc aag ctg cct tca aaa gct ttg ggc aaa ggt gtt acc gag      432
Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu
          130          135          140

gaa caa ttc aaa gag acc tgg acg agg ccg gga gct gct gga atg ggc      480
Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala Ala Gly Met Gly
145          150          155          160

gaa ggg act agc ctt gtg gtg gcc aag tcc aga atg taa      519
Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met
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<210> 32

<211> 172

- 63 -

<212> PRT

<213> *Aeromonas caviae*

<400> 32

Met Ser Ala Gln Ser Leu Glu Val Gly Gln Lys Ala Arg Leu Ser Lys
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Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser Glu Asp
 20 25 30

Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe
 35 40 45

Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly
 50 55 60

Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gln
 65 70 75 80

Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala
 85 90 95

Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu
 100 105 110

Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu
~~115~~ 120 125

Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu
 130 135 140

Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala Ala Gly Met Gly
 145 150 155 160

Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met
 165 170

<210> 33

<211> 598

- 64 -

<212> DNA

<213> *Aeromonas caviae*

<400> 33
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gacccggcct tcgcccgcac cacggcggtc gagcgggcca tagtccacgg catgctgctc 180
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gaggtgaccg cccttcgcga ggacaagccc atcgccaccc tgaccacccg catcttcacc 360
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atgggcgaag ggcgaaggga ctagccttgt ggtggccaag tccagaatgt aagacagacg 540
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<210> 34

<211> 31

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 34
nnnnnnnggat ccatggcttc tatgatatcc t 31

<210> 35

<211> 30

<212> DNA

- 65 -

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 35

nnnnnnggat ccatgactga cgttgatc

30

<210> 36

<211> 30

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 36

nnnnnnggat ccatgactca gcgcattgcg

30

<210> 37

<211> 30

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 37

- 66 -

nnnnnnggat ccatggcgac cggcaaaggc 30

<210> 38

<211> 18

<212> DNA

<213> artificial sequence

<400> 38

ctgagtcatg tccactcc

18

<210> 39

<211> 18

<212> DNA

<213> artificial sequence

<400> 39

ctgccgactg gtggaacc

18

<210> 40

<211> 18

<212> DNA

<213> ~~artificial~~ artificial sequence

<400> 40

gaagcgtcat gccttggc

18

<210> 41

<211> 27

<212> DNA

<213> artificial sequence

<220>

- 67 -

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 41

nnnnnnggat ccatgagcca gaagaac

27

<210> 42

<211> 28

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 42

nnnnnnggta cctcatcggt catgcacg

28

<210> 43

<211> 32

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 43

nnnnnncccg ggtgagccag aagaacaata ac

32

<210> 44

- 68 -

<211> 25

<212> DNA

<213> artificial sequence

<400> 44

ggatccatga gcgcacaatc cctgg

25

<210> 45

<211> 27

<212> DNA

<213> artificial sequence

<400> 45

aagcttttga aggcagcttg accacgg

27

<210> 46

<211> 27

<212> DNA

<213> artificial sequence

<400> 46

cccgggtgag gccagaaatc gctgtac

27

<210> 47

<211> 25

<212> DNA

<213> artificial sequence

<400> 47

ggtacctcag atggcaaata catgc

25

<210> 48

- 69 -

<211> 36

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 48

nngagctcga tgggaggtgc tcgaagacat attacc

36

<210> 49

<211> 26

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<223> "n" is an unknown nucleotide

<400> 49

nnggatcctg tactagatat ggcagc

26

<210> 50

<211> 38

<212> DNA

<213> artificial sequence

<400> 50

ctactcattt actagtcacc atggcgccca ccgtgatg

38

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<210> 51

<211> 35

<212> DNA

<213> artificial sequence

<400> 51

catcttactg gtacctttag tacaacggtg acgcc

35

<210> 52

<211> 39

<212> DNA

<213> artificial sequence

<400> 52

ctactcattt actagtcacc atgagcacat acgaaggtc

39

<210> 53

<211> 36

<212> DNA

<213> artificial sequence

<400> 53

catcttactg gtaccttcag cgtttatatcg cttgca

36